1646

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RAW SEQUENCE LISTING   DATE: 02/04/2002
PATENT APPLICATION: US/09/525,998A   TIME: 11:33:32

Input Set : A:\98385Eseq.txt
Output Set: N:\CRF3\02042002\I525998A.raw

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 3 <110> APPLICANT: Hauptmann, Rudolph
 4          Himmler, Adolph
 5          Maurer-Fogy, Ingrid
 6          Stratowa, Christian
 8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
   ?        Them
11 <130> FILE REFERENCE: 98-385-E
13 <140> CURRENT APPLICATION NUMBER: 09/525,998A
14 <141> CURRENT FILING DATE: 2000-03-15
16 <150> PRIOR APPLICATION NUMBER: 08/383,676
17 <151> PRIOR FILING DATE: 1995-02-01
19 <150> PRIOR APPLICATION NUMBER: 08/153,287
20 <151> PRIOR FILING DATE: 1993-11-17
22 <150> PRIOR APPLICATION NUMBER: 07/821,750
23 <151> PRIOR FILING DATE: 1993-01-02
25 <150> PRIOR APPLICATION NUMBER: 07/511,430
26 <151> PRIOR FILING DATE: 1990-04-20
28 <160> NUMBER OF SEQ ID NOS: 97
30 <170> SOFTWARE: PatentIn Ver. 2.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1368
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
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38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(1365)
41 <220> FEATURE:
42 <221> NAME/KEY: sig_peptide
43 <222> LOCATION: (1)..(87)
45 <220> FEATURE:
46 <221> NAME/KEY: misc_feature
47 <222> LOCATION: (88)..(120)
48 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
49        extracellular proteases following secretion
51 <220> FEATURE:
52 <221> NAME/KEY: misc_feature
53 <222> LOCATION: (606)..(633)
54 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
55        extracellular proteases following secretion
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59 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
60   1               5                  10                 15
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62  gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct    96
63  Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
64          20                  25                  30
66  cac cta ggg gac agg gag aag aaa gat agt gtg tgt ccc caa gga aaa    144
67  His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
68          35                  40                  45
70  tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa    192
71  Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
72          50                  55                  60
74  gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac    240
75  Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
76      65                  70                  75                  80
78  tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc    288
79  Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
80                  85                  90                  95
82  aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg    336
83  Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
84              100                 105                 110
86  gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg    384
87  Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
88              115                 120                 125
90  aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc    432
91  Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
92          130                 135                 140
94  aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag    480
95  Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
96  145                 150                 155                 160
98  aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa    528
99  Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
100                 165                 170                 175
102 aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg    576
103 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
104             180                 185                 190
106 aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca    624
107 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
108             195                 200                 205
110 ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt    672
111 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
112             210                 215                 220
114 tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag    720
115 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
116 225                 230                 235                 240
118 tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag    768
119 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
120             245                 250                 255
122 ggg gag ctt gaa gga act act act aag ccc ctg gcc cca aac cca agc    816
123 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
124             260                 265                 270
126 ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg    864
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Input Set : A:\98385Eseq.txt
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127 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
128     275             280             285
130 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt     912
131 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
132     290             295             300
134 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg     960
135 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
136 305             310             315             320
138 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gat ccc atc ccc aac     1008
139 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
140             325             330             335
142 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac     1056
143 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
144             340             345             350
146 act gat gac ccc gcg acg ctg tac gcc gtg gtg gaa aac gtg ccc ccg     1104
147 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
148     355             360             365
150 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag     1152
151 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
152     370             375             380
154 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa     1200
155 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
156 385             390             395             400
158 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc     1248
159 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
160             405             410             415
162 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc     1296
163 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
164             420             425             430
166 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg     1344
167 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
168     435             440             445
170 ccc gcg ccc agt ctt ctc aga tga     1368
171 Pro Ala Pro Ser Leu Leu Arg
172     450             455
175 <210> SEQ ID NO: 2
176 <211> LENGTH: 455
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 2
181 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
182     1               5               10              15
184 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
185             20              25              30
187 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
188             35              40              45
190 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
191     50              55              60
193 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
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Input Set : A:\98385Eseq.txt
Output Set: N:\CRF3\02042002\I525998A.raw

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194  65                       70                    75                    80
196  Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
197              85                    90                    95
199  Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
200              100                   105                   110
202  Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
203              115                   120                   125
205  Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
206          130                   135                   140
208  Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
209  145                   150                   155                   160
211  Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
212                        165                   170                   175
214  Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
215                  180                   185                   190
217  Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
218              195                   200                   205
220  Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
221          210                   215                   220
223  Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
224  225                   230                   235                   240
226  Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
227                  245                   250                   255
229  Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
230              260                   265                   270
232  Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
233          275                   280                   285
235  Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
236          290                   295                   300
238  Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
239  305                   310                   315                   320
241  Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
242                  325                   330                   335
244  Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
245              340                   345                   350
247  Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
248          355                   360                   365
250  Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
251          370                   375                   380
253  Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
254  385                   390                   395                   400
256  Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
257                  405                   410                   415
259  Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
260              420                   425                   430
262  Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
263              435                   440                   445
265  Pro Ala Pro Ser Leu Leu Arg
266          450                   455
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PATENT APPLICATION: US/09/525,998A   TIME: 11:33:32

Input Set : A:\98385Eseq.txt
Output Set: N:\CRF3\02042002\I525998A.raw

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270 <211> LENGTH: 483
271 <212> TYPE: DNA
272 <213> ORGANISM: Homo sapiens
274 <220> FEATURE:
275 <221> NAME/KEY: CDS
276 <222> LOCATION: (1)..(483)
278 <400> SEQUENCE: 3
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280 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
281  1               5                   10                  15
283 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt   96
284 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
285              20                  25                  30
287 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc  144
288 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
289          35                  40                  45
291 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa  192
292 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
293      50                  55                  60
295 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac  240
296 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
297  65                  70                  75                  80
299 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg  288
300 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
301                  85                  90                  95
303 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg  336
304 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
305              100                 105                 110
307 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc  384
308 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
309          115                 120                 125
311 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac  432
312 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
313      130                 135                 140
315 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag  480
316 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
317 145                 150                 155                 160
319 aat                                                              483
320 Asn
323 <210> SEQ ID NO: 4
324 <211> LENGTH: 161
325 <212> TYPE: PRT
326 <213> ORGANISM: Homo sapiens
328 <400> SEQUENCE: 4
329 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
330  1               5                   10                  15
332 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
333              20                  25                  30
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VERIFICATION SUMMARY   DATE: 02/04/2002
PATENT APPLICATION: US/09/525,998A TIME: 11:33:33

Input Set : A:\98385Eseq.txt
Output Set: N:\CRF3\02042002\I525998A.raw

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L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1686 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:2019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:2239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:2245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:2351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36
L:2426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:2447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2470 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:2489 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:2492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:2525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46
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